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# **Multi-Scale Brain Parcellator Documentation**

*Release 1.1.0*

**Brain Communication Pathways Sinergia Consortium**

**Oct 22, 2019**



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This pipeline is developed by the Hagmann's group at the University Hospital of Lausanne (CHUV) for use within the [SNF Sinergia Project 170873](#), as well as for open-source software distribution.



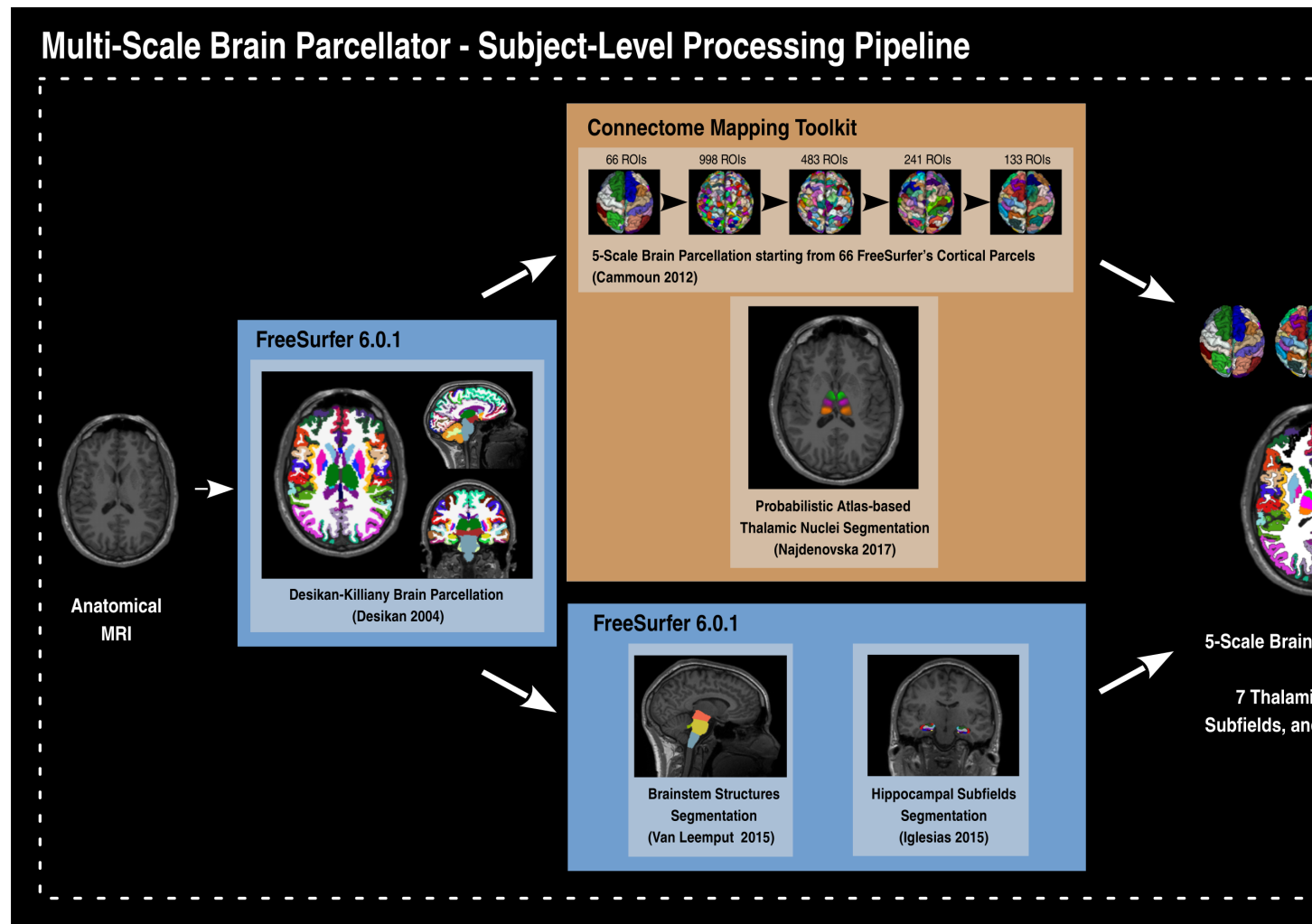
# CHAPTER 1

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## About

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Multi-Scale Brain Parcellator, part of the Connectome Mapping Toolkit (CMTK), is a BIDS App that implements a full anatomical MRI processing pipeline, from raw T1w data to structural brain parcellation at five different scales.



The `Multi-Scale Brain Parcellator` pipelines uses a combination of tools from well-known software packages, including `FSL`, `FreeSurfer`, `ANTs` as well as in-house tools from CMTK.

This tool allows you to easily do the following:

- Take T1 from raw to brain parcellations at 5 different scales.
- Implement tools from different software packages.
- Automate and parallelize processing steps, which provides a significant speed-up from typical linear, manual processing.

Reproducibility and replicability are promoted through the distribution of a BIDSApp, a software container image which provide a frozen environment where versions of all external softwares and libraries are fixed.



## CHAPTER 2

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### Funding

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Work supported by the SNF Sinergia Grant 170873 (<http://p3.snf.ch/Project-170873>).



## CHAPTER 3

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### License information

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### 4.1 Installation Instruction

**Warning:** This software is for research purposes only and shall not be used for any clinical use. This software has not been reviewed or approved by the Food and Drug Administration or equivalent authority, and is for non-clinical, IRB-approved Research Use Only. In no event shall data or images generated through the use of the Software be used in the provision of patient care.

The Multi-Scale Brain Parcellator is a BIDS App that relies on Docker. Make sure that you have Docker installed or follow the instructions found in *Installation of Docker*. Then, install the Multi-Scale Brain Parcellator by following the instructions found in *Installation of the Multi-Scale Brain Parcellator*.

#### 4.1.1 Installation of Docker

- Installed Docker Engine corresponding to your system
  - For Ubuntu 14.04/16.04/18.04, follow the instructions from the web page:

```
$ firefox https://docs.docker.com/install/linux/docker-ce/ubuntu/
```

- For Mac OSX ( $\geq 10.10.3$ ), get the .dmg installer from the web page:

```
$ firefox https://store.docker.com/editions/community/docker-ce-desktop-mac
```

- For Windows ( $\geq 10$ ), get the installer from the web page:

```
$ firefox https://store.docker.com/editions/community/docker-ce-desktop-  
↪ windows
```

**Note:** Multi-Scale Brain Parcellator BIDSApp has been tested only on Ubuntu and MacOSX. For Windows users, it might be required to make few patches in the Dockerfile.

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- For Ubuntu, Docker could be managed as a non-root user

- Open a terminal
- Create the docker group:

```
$ sudo groupadd docker
```

- Add the current user to the docker group:

```
$ sudo usermod -G docker -a $USER
```

- Reboot

After reboot, test if docker is managed as non-root:

```
$ docker run hello-world
```

### 4.1.2 Installation of the Multi-Scale Brain Parcellator

Installation and use of the Multi-Scale Brain Parcellator has been facilitated through the distribution of a Docker container image.

- Open a terminal
- Get the latest release of the BIDS App:

```
$ docker pull sebastientourbier/multiscalebrainparcellator:latest
```

- To display all docker images available:

```
$ docker images
```

You should see the docker image “multiscalebrainparcellator” with tag “latest” is now available.

### Help/Questions

If you run into any problems or have any questions, you can post to the [CMTK-users group](#). Code bugs can be reported by creating a “New Issue” on the [source code repository](#).

## 4.2 Usage

### 4.2.1 Execution and the BIDS format

The Multi-Scale Brain Parcellator workflow takes as principal input the path of the dataset that is to be processed.

The input dataset is required to be in valid BIDS (Brain Imaging Data Structure) format, and it must include at least one T1w or MPRAGE structural image. For example:

```

ds-example/

  README
  CHANGES
  participants.tsv
  dataset_description.json

  sub-01/
    anat/
      sub-01_T1w.nii.gz
      sub-01_T1w.json

  ...

  sub-<subject_label>/
    anat/
      sub-<subject_label>_T1w.nii.gz
      sub-<subject_label>_T1w.json
    ...
  ...

```

For more information about BIDS, please consult the [BIDS Website](#) and the [Online BIDS Specifications](#). [HeuDiConv](#) can assist you in converting DICOM brain imaging data to BIDS. A nice tutorial can be found @ [BIDS Tutorial Series: HeuDiConv Walkthrough](#).

---

**Important:** We highly recommend that you validate your dataset with the free, online [BIDS Validator](#).

---

## 4.2.2 Commandline Arguments

The command to run Multi-Scale Brain Parcellator follow the [BIDS-Apps](#) definition with additional options specific to this pipeline.

Multi-scale Brain Parcellator BIDS App.

```

usage: multiscalebrainparcellator [-h]
                                [--participant_label PARTICIPANT_LABEL [PARTICIPANT_
↪ LABEL ...]]
                                [--multiproc_number_of_cores MULTIPROC_NUMBER_OF_
↪ CORES]
                                [--number_of_participants_processed_in_parallel_
↪ NUMBER_OF_PARTICIPANTS_PROCESSED_IN_PARALLEL]
                                [--fs_number_of_cores FS_NUMBER_OF_CORES]
                                [--fs_license FS_LICENSE]
                                [--isotropic_resolution ISOTROPIC_RESOLUTION]
                                [--thalamic_nuclei]
                                [--hippocampal_subfields]
                                [--brainstem_structures]
                                [--skip_bids_validator] [-v]
                                bids_dir output_dir {participant}

```

### Positional Arguments

|                 |  |
|-----------------|--|
| <b>bids_dir</b> | The directory with the input dataset formatted according to the BIDS standard. |
|-----------------|--|

|                       |  |
|-----------------------|--|
| <b>output_dir</b>     | The directory where the output files should be stored. If you are running group level analysis this folder should be prepopulated with the results of the participant level analysis.  |
| <b>analysis_level</b> | Possible choices: participant<br><br>Level of the analysis that will be performed. Note that only participant level analysis is available. Multiple participant level analyses can be run independently (in parallel) using the same output_dir. |

## Named Arguments

|   |   |
|---|---|
| <b>--participant_label</b>                            | The label(s) of the participant(s) that should be analyzed. The label corresponds to sub-<participant_label> from the BIDS spec (so it does not include “sub-“). If this parameter is not provided all subjects should be analyzed. Multiple participants can be specified with a space separated list. |
| <b>--multiproc_number_of_cores</b>                    | The number of cores to be used by the MultiProc plugin of Nipype (One core used by default).  |
| <b>--number_of_participants_processed_in_parallel</b> | The number of subjects to be processed in parallel (One core used by default).  |
| <b>--fs_number_of_cores</b>                           | The number of cores to be used by Freesurfer (One core used by default).  |
| <b>--fs_license</b>                                   | Path to Freesurfer license.   |
| <b>--isotropic_resolution</b>                         | The isotropic resolution in mm used to resample the original anatomical images and applied at the beginning of the processing pipeline.   |
| <b>--thalamic_nuclei</b>                              | Whether or not to parcellate the thalamic nuclei.<br><br>Default: False   |
| <b>--hippocampal_subfields</b>                        | Whether or not to parcellate the hippocampal subfields.<br><br>Default: False   |
| <b>--brainstem_structures</b>                         | Whether or not to parcellate the brainstem structures.<br><br>Default: False  |
| <b>--skip_bids_validator</b>                          | Whether or not to perform BIDS dataset validation.<br><br>Default: False  |
| <b>-v, --version</b>                                  | Display the version of Multi-scale Brain Parcellator BIDS-App.  |

### See also:

More information about BIDS Apps? Please check directly on the [BIDS Apps Website](#).

## 4.2.3 Participant Level Analysis

To run the docker image in participant level mode (for one participant):

```
$ docker run -it --rm \
-v /home/localadmin/data/ds-example:/bids_dir \
-v /media/localadmin/data/ds-example/derivatives:/output_dir \
-v /usr/local/freesurfer/license.txt:/bids_dir/code/license.txt \
sebastientourbier/multiscalebrainparcellator:v1.1.0 \
```

(continues on next page)



(continued from previous page)

```
/bids_dir /output_dir participant --participant_label 01 \  
--isotropic_resolution 1.0 \  
--thalamic_nuclei \  
--hippocampal_subfields \  
--brainstem_structures
```

---

**Important:** The local directory of the input BIDS dataset (here: `/home/localadmin/data/ds001`) and the output directory (here: `/media/localadmin/data/ds001/derivatives`) used to process have to be mapped to the folders `/bids_dir` and `/output_dir` respectively using the `-v` docker run option.

---

---

**Important:** Multi-scale brain parcellator needs your own **Freesurfer** license. As a result, you must map your license (for instance `/usr/local/freesurfer/license.txt`) to the file `/bids_dir/code/license.txt` inside the BIDS App.

---

## 4.2.4 Debugging

Logs are outputted to `sub-<participant_label>_log-multiscalebrainparcellator.txt` located in `<output_dir>/cmp/sub-<participant_label>/` directory.

## 4.2.5 Support and communication

The documentation of this project is found here: <http://multiscalebrainparcellator.readthedocs.org/en/latest/>.

All bugs, concerns and enhancement requests for this software can be submitted here: <https://github.com/sebastientourbier/multiscalebrainparcellator/issues>.

If you run into any problems or have any questions, you can post to the [CMTK-users](#) group.

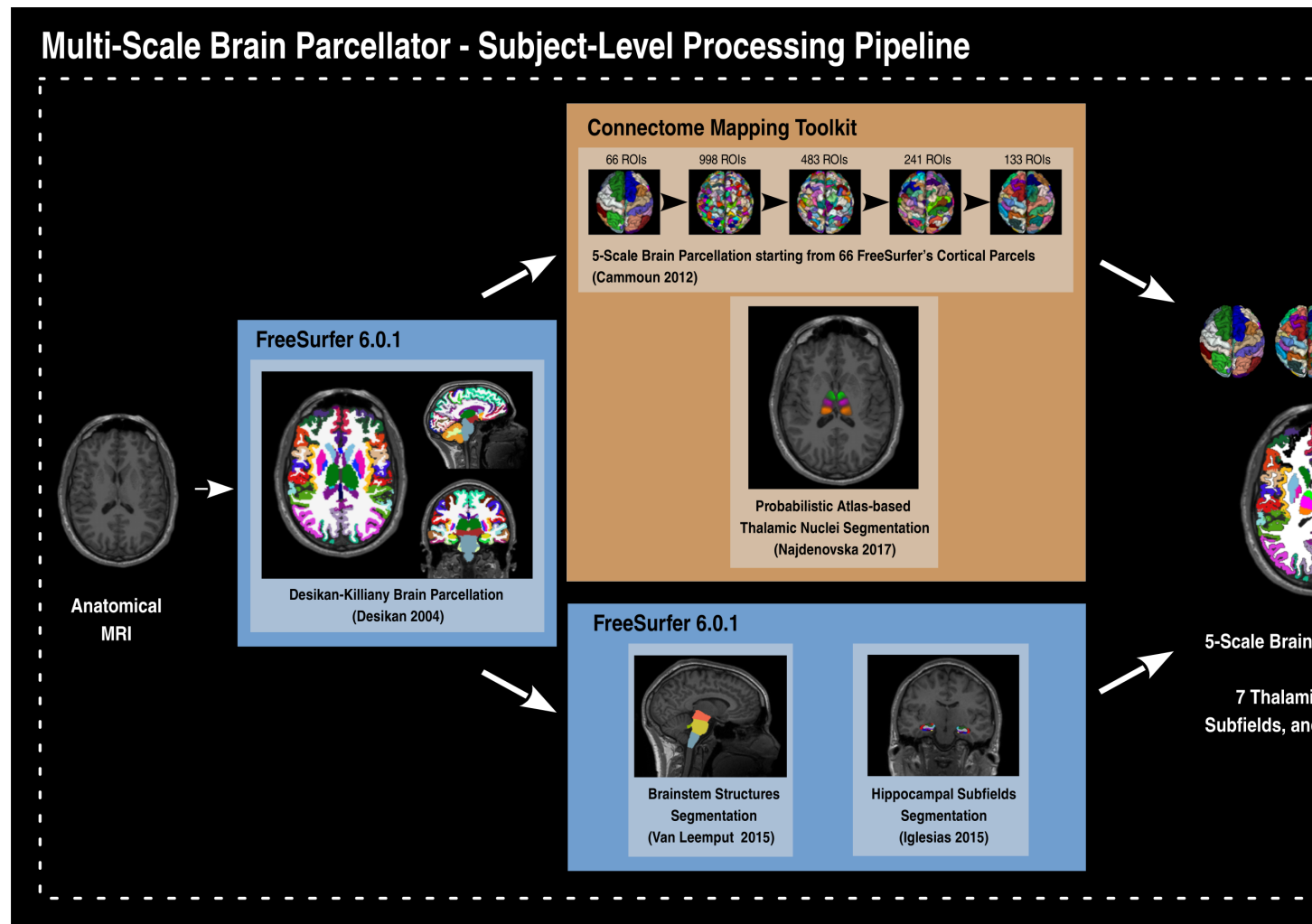
## 4.2.6 Not running on a local machine? - Data transfer

If you intend to run `multiscalebrainparcellator` on a remote system, you will need to make your data available within that system first. Comprehensive solutions such as [Datalad](#) will handle data transfers with the appropriate settings and commands. Datalad also performs version control over your data.

# 4.3 Processing Pipeline Details

## 4.3.1 Workflow

The Multi-Scale Brain Parcellator pipelines uses a combination of tools from the well-known software packages [FSL](#), [FreeSurfer](#), [ANTs](#) as well as in-house tools from the Connectome Mapping ToolKit (CMTK).

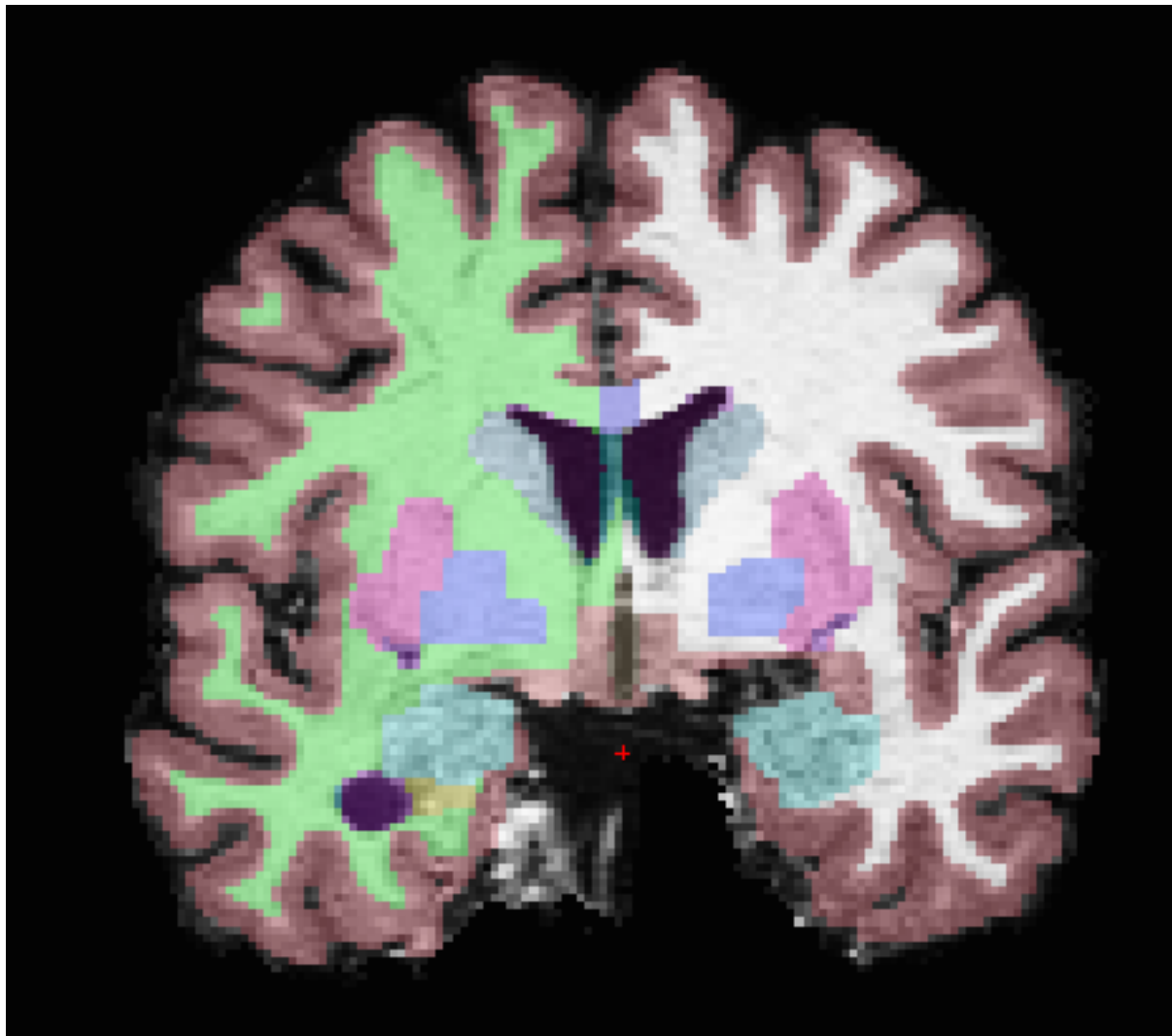


### 4.3.2 Segmentation

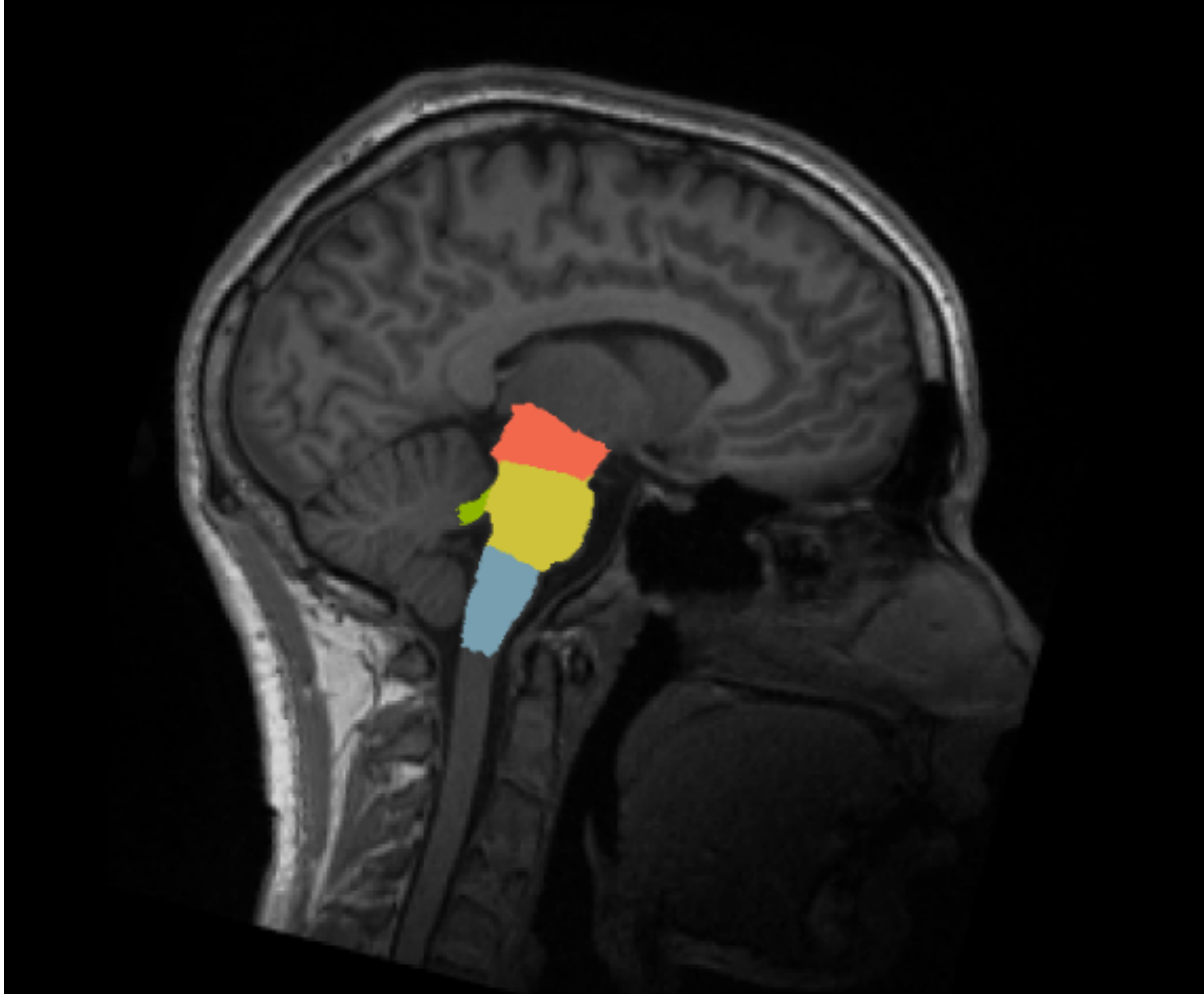
Surfaces are extracted using Freesurfer.



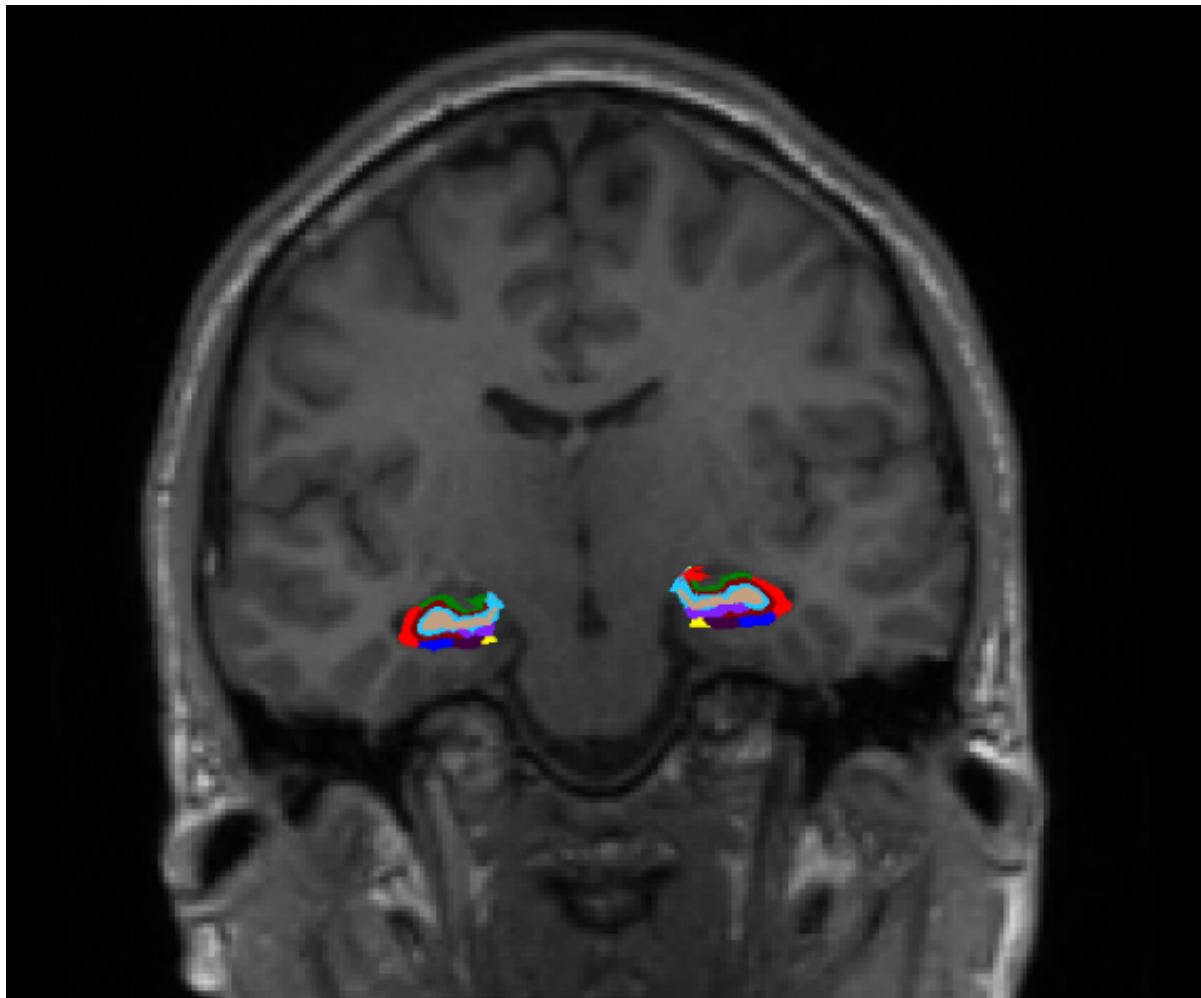
T1 is segmented using Freesurfer.



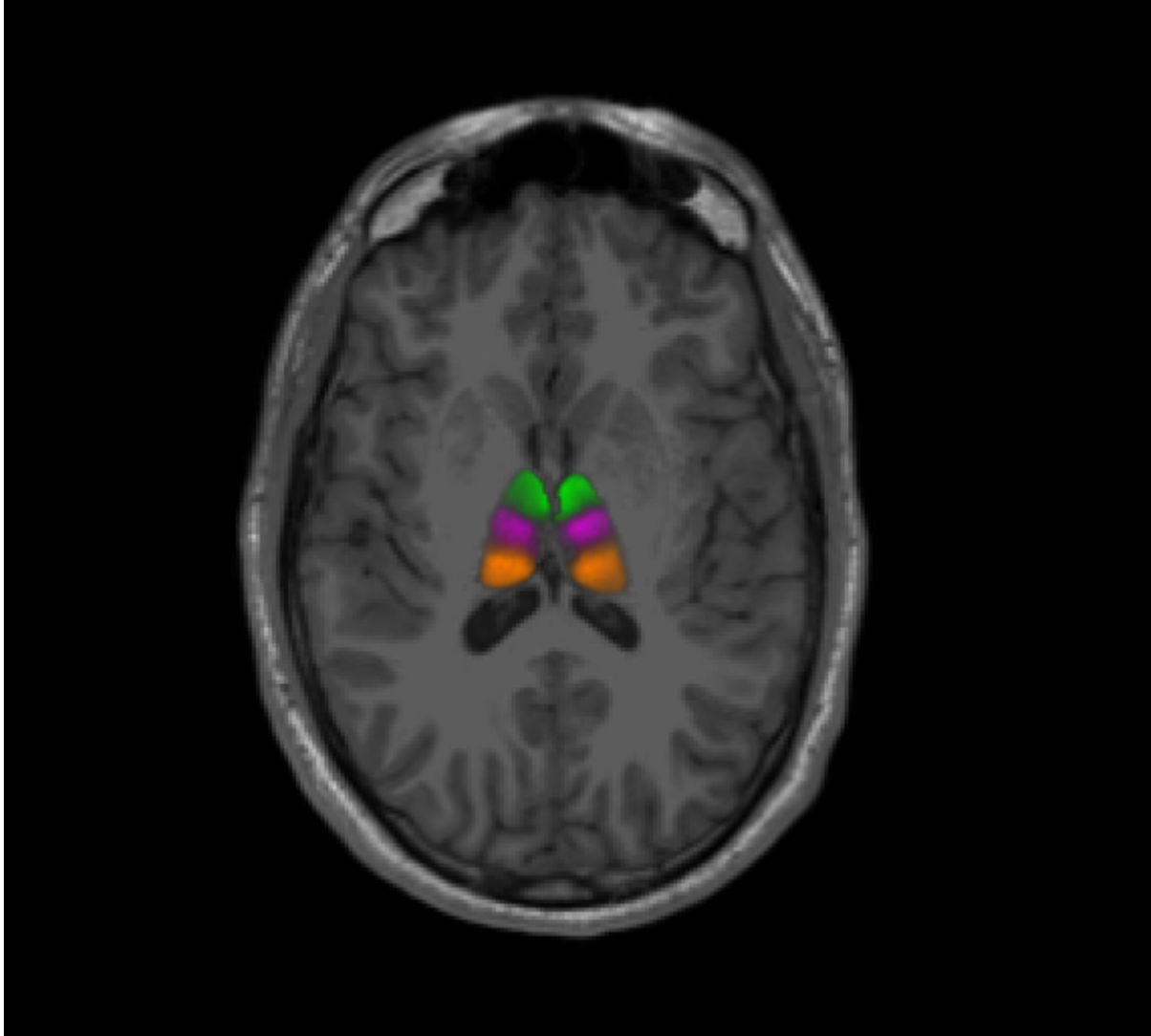
Brainstem sub-structures are segmented using Freesurfer.



Hippocampal subfields are segmented using Freesurfer.

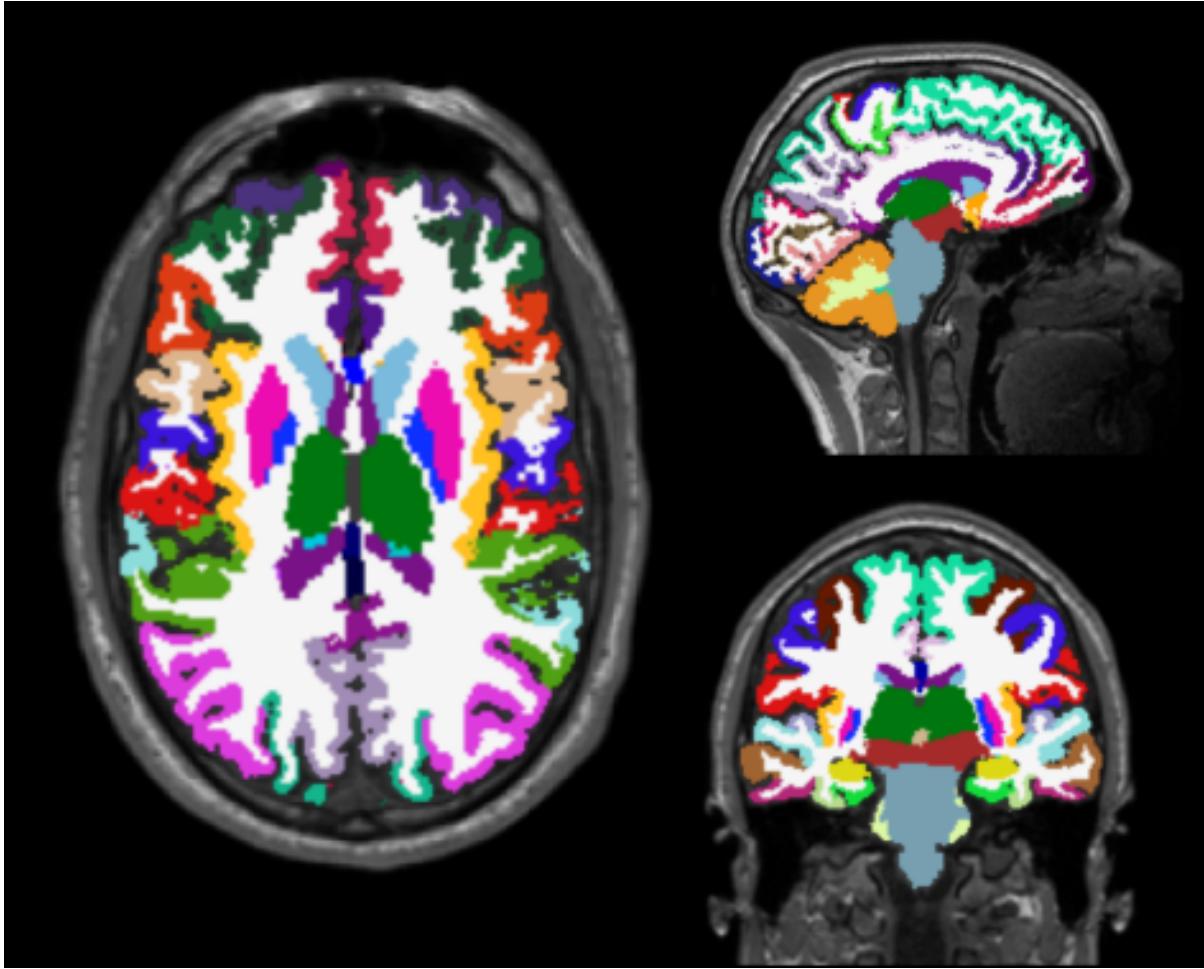


Thalamic nuclei are segmented using an in-house tool of CMTK which implement the probabilistic atlas-based thalamic segmentation method with the help of ANTs (See Najdenovska 2018 in Citing Section).



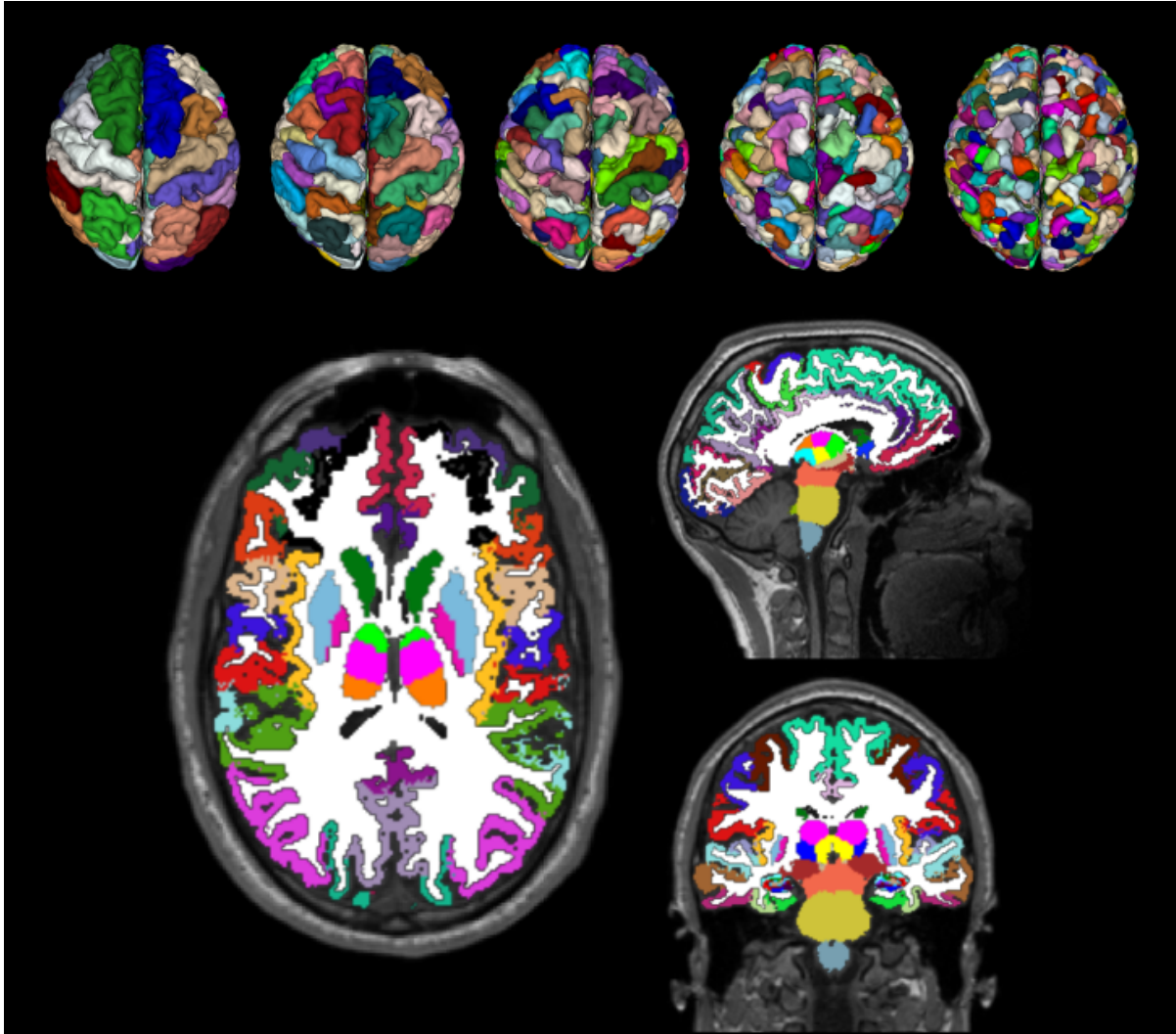
### Parcellation

Desikan-Killiany brain parcellation is performed using Freesurfer.



5-Scale Brain parcellation is created according to Cammoun et al. 2012 (See `Citing`) at 5 different scales. All structures are then combined to create the final brain parcellation at each scale.





## 4.4 Outputs of Multi-Scale Brain Parcellator

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**Note:** Multi-Scale Brain Parcellator outputs are currently being updated to conform to the BIDS Common Derivatives specification (see [BIDS Common Derivatives Extension](#)).

---

### 4.4.1 Multi-Scale Brain Parcellator Derivatives

Processed, or derivative, data are written to `<bids_dataset/derivatives>/cmp/sub-<subject_label>`. In this folder, a configuration file generated and used for processing each participant is saved as `sub-<subject_label>_anatomical_config.ini`. It summarizes pipeline workflow options and parameters used for processing.

Anatomical derivatives in the original T1w space are placed in each subject's `anat` subfolder including:

- `anat/sub-<subject_label>_desc-head_T1w.nii.gz`
- `anat/sub-<subject_label>_desc-brain_T1w.nii.gz`

- anat/sub-<subject\_label>\_desc-brain\_mask.nii.gz
- anat/sub-<subject\_label>\_label-WM\_dseg.nii.gz
- anat/sub-<subject\_label>\_label-GM\_dseg.nii.gz
- anat/sub-<subject\_label>\_label-CSF\_dseg.nii.gz

The five different brain parcellation are saved as:

- anat/sub-<subject\_label>\_label-L2018\_desc-<scale\_label>\_atlas.nii.gz

where <scale\_label> : scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale.

Additionally, the description of parcel labels and the updated FreeSurfer color lookup table are saved as:

- anat/sub-<subject\_label>\_label-L2018\_desc-<scale\_label>\_atlas.graphml
- anat/sub-<subject\_label>\_label-L2018\_desc-<scale\_label>\_atlas\_FreeSurferColorLUT.txt

Finally, parcel volumetry results for each scale are saved in a TSV file as:

- anat/sub-<subject\_label>\_label-L2018\_desc-<scale\_label>\_stats.tsv

### 4.4.2 FreeSurfer Derivatives

A FreeSurfer subjects directory is created in <bids\_dataset/derivatives>/freesurfer.

```
freesurfer/  
  fsaverage/  
    mri/  
    surf/  
    ...  
  sub-<subject_label>/  
    mri/  
    surf/  
    ...  
  ...
```

The fsaverage subject distributed with the running version of FreeSurfer is copied into this directory.

## 4.5 BSD 3-Clause License

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## 4.6 Citing

### Important:

- If you are using Multi-Scale Brain Parcellator in your work, please acknowledge this software and its dependencies. To help you to do so, we recommend you to use, modify to your needs, and include in your work the following text:

*Results included in this manuscript come from the Connectome Mapper 3 version latest [1,2], a processing pipeline, written in Python which uses Nipype [3,4]. It is encapsulated in a BIDS app [5] based on Docker [6] and Singularity [7] container technologies. Resampling to isotropic resolution, Desikan-Killiany brain parcellation [8], brainstem parcellation [9], and hippocampal subfields segmentation [10] were performed using FreeSurfer 6.0.1. Final parcellations were created by performing cortical brain parcellation on at 5 different scales [11], probabilistic atlas-based segmentation of the thalamic nuclei [12], and combination of all segmented structures, using in-house CMTK tools and the antsRegistrationSyNQuick tool of ANTS v2.2.0 [13].*

### References

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2. Tourbier S, Aleman-Gomez Y, Griffa A, Bach Cuadra M, Hagmann P (2019, June 12). Multi-Scale Brain Parcellator: a BIDS App for the Lausanne Connectome Parcellation. 25th Annual Meeting of the Organization for Human Brain Mapping (OHBM), abstract #1714, poster #W616.
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- 

#### 4.6.1 Poster

- Organization for Human Brain Mapping 2019 ([Abstract](#); [Poster](#))



# W616 - Multi-Scale Brain Parcellator: a BIDS App for the Lausanne Connectome Parcellation

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## MOTIVATION

- **Multi-Scale Brain Parcellator:** independent tool developed in parallel of the development of the Connectome Mapper 3 (CMP3) [1, [connectomics.org](https://connectomics.org)].
- Implement a 5-scale brain gray matter parcellation [2] derived from the Desikan-Killiany atlas [3] and extended with new structures including a subdivision of the thalamus into 7 nuclei [4], the hippocampus into 12 subfields [5] and the brainstem into 4 sub-structures [6].
- Such a brain parcellation can serve many add on applications such as volumetry, definition of regions of interest for tractography or functional connectivity analysis.

## AIMS

- Support datasets with Brain Imaging Data Structure (BIDS) format [7]
- Adopt frameworks that have proven to be capable of effective large scale collaboration
- Make the multi-scale parcellation of CMP3 standalone, accessible, portable, interoperable and easy-to-use

## THE PIPELINE

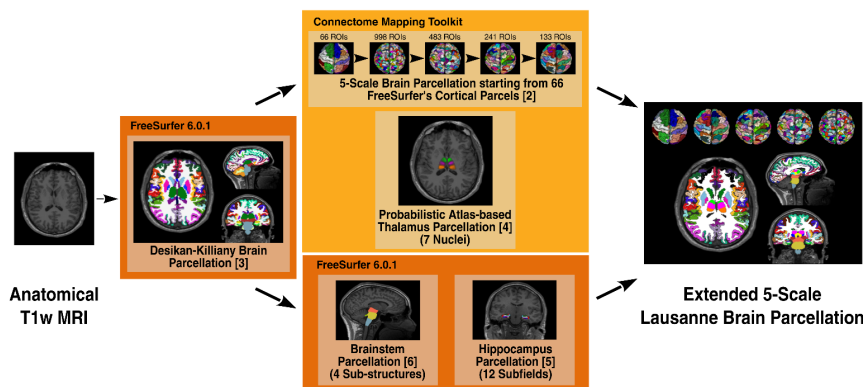


Figure 1: Overview of the Multi-Scale Brain Parcellator processing pipeline. ANTs 2.2.0 [8] is used for linear and symmetric diffeomorphic (SyN) registration.

## PROCESSED DATA (DERIVATIVES)

### Multi-Scale Brain Parcellator Derivatives

- Derivatives written to `<bids_dataset/derivatives>/cmp/sub-<subject_label>/`
- Pipeline options and parameters summarized in a configuration `.ini` file:

## 4.6. Citing

`sub-<subject_label>_anatomical_config.ini`

- Anatomical derivatives in the original T1w space saved in each subject's `anat` subfolder:

- `anat/sub-<subject_label>_desc-head_T1w.nii.gz`
- `anat/sub-<subject_label>_desc-brain_T1w.nii.gz`
- `anat/sub-<subject_label>_desc-brain_mask.nii.gz`
- `anat/sub-<subject_label>_label-WM_desc.nii.gz`

## ARCHITECTURE

- Pipeline of the Multi-Scale Brain Parcellator is written to interface with FreeSurfer and CMTK (Connectome Mapper Toolkit) workflow.
- Encapsulated in a BIDS App [10], a framework based on Docker [11] and Singularity [12] on HPC → promotes

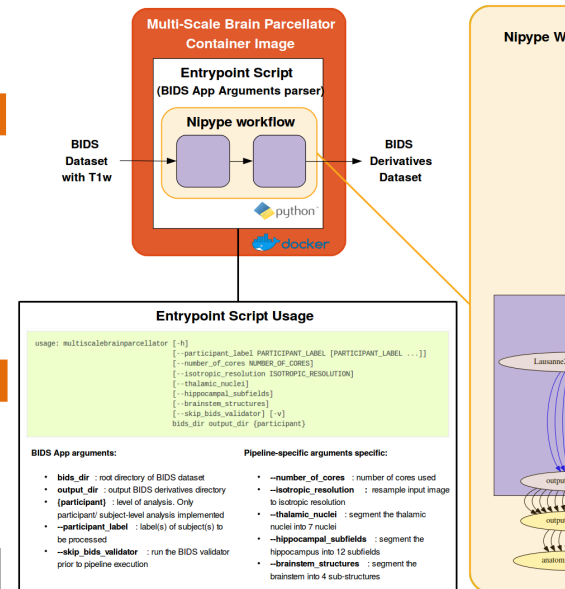


Figure 2: Architecture of Multi-Scale Brain Parcellator

## BIDS App Development and Versioning

- Multi-scale Brain Parcellator uses CircleCI for Continuous Integration

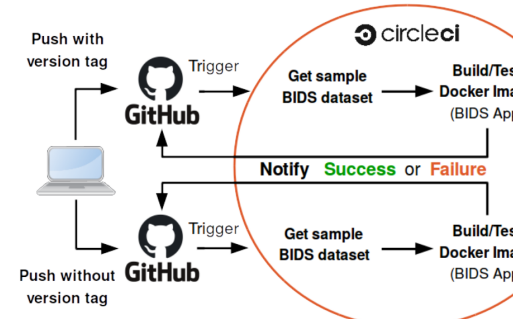


Figure 3: Continuous integration flow for the development of Multi-Scale Brain Parcellator. Each change committed to GitHub triggers a "build and test" on CircleCI. When ready to release a version, a push to GitHub repository. A version tag will not only trigger a build and test but also deploy the new "tagged" docker image to Docker Hub.

## 4.7 Contributing

Coming